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GenCore version 4.5
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OM protein - protein search, using sw model

March 14, 2001, 16:12:48 ; Search time 12.3 Seconds
(without alignments)
1191.993 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-455-486-6 2351 1 MESISMMGSPKSLSETCLPN......ALVLPSIVILDLLQLCRYPD 454

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 88757 seqs, 32294092 residues Searched:

88757

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_39:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

		đ		•	SUMMARIES		
Result		Query					-
NO.	Score	Match	Length	DB	ΩI	Description	
н	133		223		4	36 me	
7	120.5	δ.	232	-	F4RE_METTH	_	
3	111.5	4	695		FSHR_MACFA	12	7 3
4	109	4	693		FSHR_CHICK	gallus	
2	109	4	712		FRE6_YEAST	sacchai	۲)
9	107.5	4	629		FRE7_YEAST	Q12333 saccharomyc	
7	107.5	4	695		FSHR_HUMAN	P23945 homo sapien	_
80	104.5	4	695		FSHR_PIG	s sns	
6	104	4.4	396		YDEA_ECOLI	esch	æ
10	103	4	465		NPT1_MOUSE	Q61983 mus musculu	٦.
11	100	4	476		RF3_SACBA	sacc	7)
. 12	99.5	4	452		NU4M_BRALA	079421 branchiosto	0
13	66	4.2	365		GP68_HUMAN	Q15743 homo sapien	
14	86	4	3411		POLG_YEFV1	y gen	0
15	86	4.	3411		POLG_YEFV2	y genome	0
16	97.5	4	695		FSHR_BOVIN	P35376 bos taurus	
17	4	4	692	П	FSHR_RAT	P20395 rattus norv	>
18	96.5	4	989	Н	FRE1_YEAST		c)
19	96	4	261	7	PHSC_ECOLI		с
20	95	4	393	7	NUCC_ARATH	arabidopsi	ß
21	94.5	4	492	П	SECY_CYAPA		
22	94.5	4	695	П	FSHR_SHEEP		
23	93.2		452	П	NU4M_BRAFL		0
24	93.5	4	499	7	GSHR_PLAF7	O15770 plasmodium	
25	. 93.5	4	1233	Н	VL1_REOVD		ப
26	93	4	388		HMC3_DESVH	P33390 desulfovibr	<u>د</u>
27	93	4	459		NU4M_BOVIN	P03910 bos taurus	
28	93	4	521		YT25_CAEEL	caenor	
		m	490	Н	GTR1_CHICK	P46896 gallus gall	_
30.		ω.	883		YHL6_YEAST	sacchai	()
31	92.5	m.	1769		YJK9_YEAST	P42945 saccharomyc	Ð
32	92.5	'n	2037	7	FAS1_CANAL	c fatty	
. 33	91.5	3.	495	г	TPS1_YEAST	Q00764 s alpha, alp	۵.

34 91.5 3.9 1694 1 CLH_DICDI 35 90.5 3.8 445 1 SVDL_YEAST 36 90.5 3.8 445 1 VPNP_BACSU 37 90.5 3.8 465 1 NPTL_RAT 39 90.5 3.8 564 1 KR11_YEAST 40 90 3.8 564 1 KT1_YEAST 41 89.5 3.8 345 1 YTMM_BACSU 42 89.5 3.8 345 1 NUZM_XENLA 44 89.5 3.8 345 1 NUZM_XENLA 44 89.5 3.8 433 1 YEL4_YEAST 45 89.5 3.8 687 1 FSHR_EQUAS 45 89.5 3.8 687 1 FSHR_EQUAS ALIGNMENTS ALIGNMENTS ALIGNMENTS ALIGNMENTS ALIGNMENTS ALIGNMENTS ACCOREA ACCOREA ALIGNMENTS ACCOREA ACCOREA ALIGNMENTS ACCOREA AC	91.5 3.9 1694 1 CLH_DICDI 91 3.9 458 1 SSU1_YEAST 90.5 3.8 445 1 YPNP_BACSU 90.5 3.8 465 1 NPTL_RAT 90.5 3.8 560 1 KR11_RAT 90.5 3.8 560 1 KR11_RAT 90.5 3.8 564 1 HYTC_YEAST 90.5 3.8 345 1 NUZM_EACSU 89.5 3.8 345 1 NUZM_ERLUA 89.5 3.8 345 1 NUZM_ERLUA 89.5 3.8 433 1 YBL4_YEAST 89.5 3.8 687 1 FSHR_EQUAS 89.5 3.8 687 1 FSHR_EQUAS 89.5 3.8 587 1 FSHR_EQUAS 89.5 3.8 71 FSHR_EQUAS 89.5 3.8 71 FSHR_EQUAS							Q95179 equus asinu	P38211 saccharomyc	P12132 oryza sativ	079671 pelomedusa	P03894 xenopus lae	034931 bacillus su	P39924 saccharomyc	P32893 saccharomyc	Q62795 rattus norv	P54181 bacillus su	P41930 saccharomyc	P25870 dictyosteli
91.5 3.9 169 91.5 3.9 169 90.5 3.8 46 90.5 3.8 56 90.5 3.8 23 89.5 3.8 34 89.5 3.8 43 89.5 3.8 43 89.5 3.8 43 89.5 3.8 78 89.5 3.8 78 89.5 1.00v-1997 (Rel. 35,	91.5 3.9 1694 1 CLH 90.5 3.8 445 1 YPN 90.5 3.8 445 1 YPN 90.5 3.8 560 1 KRI 90.5 3.8 564 1 HXT 89.5 3.8 345 1 YTM 89.5 3.8 345 1 NUZ 89.5 3.8 745 1 NUZ	update)		223 AA.			MENTS	JAS	\ST	SA	nsr	1LA	Su	YST	YST	٠.	SU	'ST	10
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91.5 3.9 169 91.5 3.9 169 90.5 3.8 46 90.5 3.8 56 90.5 3.8 23 89.5 3.8 34 89.5 3.8 43 89.5 3.8 43 89.5 3.8 43 89.5 3.8 78 89.5 3.8 78 89.5 1.00v-1997 (Rel. 35,	91.5 3.9 169 90.5 3.8 46 90.5 3.8 46 90.5 3.8 56 90.5 3.8 56 89.5 3.8 34 89.5 3.8 843 89.5 3.8 68 89.5 3.8 68	Creat Last	Creat	<u>،</u>				7 1	3	3	1	5	5 1	4	0	2	5	8	1
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34 91.5 35 90.5 37 90.5 38 90.5 38 90.5 40 90.5 41 89.5 43 89.5 44 89.5 45 89.5 45 89.5 45 89.5 45 89.5 47 89.5 48 89.5 49.5 41 89.5 42 89.5 43 89.5 45 89.5 45 89.5	34 91.5 35 90.5 37 90.5 38 90.5 39 90.5 40 89.5 44 89.5 44 89.5 45 89.5 45 89.5 45 89.5 46 89.5 47 89.5 48 89.5	(Rel.	(Rel.	ST				ω ω	3,8	3.8	3.8	3.8	3.8	3.8	3.8	3.8	3.8	3.9	3.9
34 35 35 36 37 39 40 40 41 42 43 43 43 45 80LT FART	34 35 36 36 39 40 40 42 43 44 44 45 44 45 45 47 47 48 48 48 48 48 48 48 48 48 48 48 48 48	NOV-1997	896; NOV-1997	E_METJA	JA	-		89.5	89.2	89.2	89.5	89.5	06	90.5	90.5	90.5	90.5	91	91.5
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FSHR_MACFA
                                                                                                                                                                                                                                                                 RECEPTOR).
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                                                                                                                                                                       FSHR_MACFA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                       -- SNNMRINQYPE-SNAEYL 133
                                                                                        ASLFPDSLIVKGFNVVSAWALQLGPKDASRQVYICSNNIQARQQVIELARQLNFI-PIDL 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -DALTKINIIFVAIH-REHYTSLWDLRHLLVGKILIDVS------NNMRINQYPESN 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteriol. 179:7135-7155(1997).

FUNCTION: CATALYSES THE REDUCTION OF F420 WITH NADP(+) AND THE REDUCTION: CATALYSES THE REDUCTION OF NADP(+) WITH F420H(2). PROBABLY COUPLES THE NADP DEPRENDENT OXIDATION OF THE ALCOHOL TO THE ALDEHYDE WITH DE F420-DEPENDENT REDUCTION OF CO(2) TO METHANE (ANABOLIC FUNCTION) (BY
                                                                                                                                                                                                                                                                                                                                                                                                                         Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois, Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K., Harison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D., Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R., Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S., McDougail S., Shimer G., Goyal A., Pietrovski S., Church G.M., Danleis C.J., Mao J.-I., Rice P., Nolling J., Reeve J.N., "Complete genome sequence of Merhanobacterium thermoautotrophicum deltaH: functional analysis and comparative genomics.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTGDQGFGLALRLAK-NNKIIIGSRKKEKAEEAAKKAKEILKQRGIEADIIGLENKDAAK
                                                            EGDVVILSLPYEYTLSTIKQLKEELKGKIVVSIGVPLATAIGDKPTRLLFPPDGSVAEMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30 KVTVGVIGSGDFAKSLTIRLIRCGYHVVIGSRNPKFASEFFPHVVDVTHHE------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CATALYTIC ACTIVITY: NADPH + COENZYME F420 = NADP(+) + REDUCED
                                                                                                                                                                                                                                                                                                                                             Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: TO M.ORGANOPHILUM F420-DEPENDENT NADP REDUCTASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein; Oxidoreductase; NADP.
SEQUENCE 232 AA; 24539 MW; AlCEGOABC8474296 CRC64;
                                                                                                                                                                                                                                                              15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
PUTATIVE F420-DEPENDENT NADP REDUCTASE (EC I.-.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5.1%; Score 120.5; DB 23.8%; Pred. No. 0.052;
                                                                                                                                                                                                                                       232 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KTNIIFVAIHREH-YTSLWDLRHLLVGKILIDV--
                                                                                                                                           GSLSSAREIENLPLRLFTLWRGPVVVAISL 222
                                                                                                                                                           send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                 Methanobacterium thermoautotrophicum
                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-98037514; PubMed-9371463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42;
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::
                                                                                                                                                                                                                                                                                                                                                            Methanobacterium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COENZYME
                                                                                                                                                                                                                                     F4RE_METTH
026350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                         AEYLASLF---PDSLIVKGFNVVSAWALQLGPKDASRQVYICSNNIQARQQVIELARQLN 186
                                                                                                                  67 PDAAASADVVVLTVPLQAQMVTLASIRDQVRDKVLIDATVPIDSCIGGSAVRYIDLWEGS 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-0CT-1993 (Rel. 27, Last sequence update)
01-0CT-2000 (Rel. 40, Last annotation update)
FOLLICLE STIMULATING HORMONE RECEPTOR PRECURSOR (FSH-R) (FOLLITROPIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: INTEGRAL MEWBRANE PROTEIN.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
FSH/LSH/TSH SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FOLLICLE STIMULATING HORMONE RECEPTOR. EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Glycoprotein; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gromoll J., Dankbar B., Sharma R.S., Nieschlag E.; "Molecular cloning of the testicular follicle stimulating horm receptor of the non human primace Macaca fascicularis and identification of multiple transcripts in the testis."; Biochem. Biophys. Res. Commun. 196:1066:1072(1993).

-1- FUNCTION: RECEPTOR FOLLICLE STIMULATING HORMORE THE A OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  695 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1. PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1. G_protein_RECEP_F1_2; 1. G_protein_coupled_receptor; Transmembrane; Phosphorylation; Repeat; Leucine-repeat.
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                                                                                                                                                                                                                                                       FI-PIDLGSLSSAREIENLPLRLFTL 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=94071854; PubMed=7504463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Rel. 27, Created)
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PRINTS; PR01143; FSHRECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X74454; CAA52463.1; -.
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PFAM; PF00560; LRR; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PF01462; LRRNT; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JN0898
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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POTENTIAL.
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                                             MEDLINE=97473503; PubMed=9332357;
                                                                                                                                                                                                                                                                                                                    EMBL; D87871; BAA13487.1; -. EMBL; U51097; AAC60030.1; -. HSSP; P23945; IXUN. GCRDB; GCR_1077; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Repeat;
                                                                                                                                                                                                                                                                                                                                                                                  INTERPRO; IPR002131; -.
INTERPRO; IPR002272; -.
PFAM; PF00001; 7tm_1; 1.
PFAM; PF00560; LRR; 2.
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INTERPRO; IPRO00276; -.
INTERPRO; IPRO01611; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     457 VYTLTAITLERWHTITHAMQLDCKVHVRHAASVMVMGWIFAFAAALFPIFGISSYMKVSI 516
                                                                                                                                                                                                                                                                                                                                                                                                              ----LLSFFFAMVHVA------YSLCLPMRRSERYLFLNMAYQQVHANIENS 348
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                                                                                                                                                                                                                                                                                                                                                                          ----KILIDVSNNMR 121
                                                                                                                                                                                                                                                             122 INQYPESNAEYLASLFPDSLIVKGFNVVSAWALQLGPKDASRQVYICSNNIQARQQVIEL 181
                                                                                                                                                                                                                                                                                                  ARQLNFIPIDLGSLSSAREIENLPLRLFTLWRGPVVVAISLATFFFLYSFVRDVIHPYAR 241
                                                                                                                                                                                                                                                                                                                                                        247 RSTYNLKKLP----SLEKLVALMEASLTYPSHCCAFANWRRQISELHPICNKSILRQEV 301
                                                                                                                                                                                                                                                                                                                                                                                           DYMTQTRGQRSSLAEDNESSYSRGFDMTYAEFDYDLCNEVVDVTCSPKPDAFNPCEDILG 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FSHR_CHICK STANDARD; PRT; 693 AA.
P79763; 090719;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
FOLLICLE STIMULATING HORMONE RECEPTOR PRECURSOR (FSH-R) (FOLLITROPIN
                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                        :| :| :: : | |:| |:| 362 YNILRVLIWFISILAITGNITULVTLTTSQYKLTVP-----RFLMCNLAFAD-----
                                                                                                                                                                                                                                                                                IH-----TIERNSFVGLSFESVILWL----NKNGIQEIHNCA-------
                                                                    6 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

7 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

N.LINKED (GLCNAC. .) (POTENTIAL).

BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                      Indels 183;
                                                                                                                                                                                   Length 695;
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                SIMILARITY.
0D60A233729B5250 CRC64;
                                            EXTRACELLULAR (POTENTIAL) 5 (POTENTIAL).
         3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
                                                    S (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                   4.7%; Score 111.5; DB 1;
17.0%; Pred. No. 0.83;
tive 75; Mismatches 151;
                                                                                                                                                                                     DB 1;
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695 AA;
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Matches
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FSHR_CHICK
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                                                                                                                                 Wakabayashi N., Suzuki A., Hoshino H., Nishimori K., Mizuno S.;
"The cDNA cloning and translent expression of a chicken gene encoding
a follicle-stimulating hormone receptor.";
Gene 197:121-127(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                         ADENYLATE CYCLASE.
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
FSH/LSH/TSH SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FOLLICLE STIMULATING HORMONE RECEPTOR EXTRACELLULAR (POTENTIAL).
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PRINTS; PR01373; GLYCHORMONER.
PRINTS; PR01143; FSHREGEPTOR.
PROSITE; PS00237; G_PROTEIN_RECEP_FL_1; I.
PROSITE; PS50262; G_PROTEIN_RECEP_FL_2; I.
G_protein coupled receptor: Transmembrane; Glycoprotein; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BY SIMILARITY.

"LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     285 DRS-GILAFTQFPLIIIFTARNSFLEFLTGVKFNSF-----ISFHKWIGRIMVLNATI 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FERRIC REDUCTASE TRANSMEMBRANE COMPONENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----WDLRHLLVGKILIDVSNNMRINQYPESNAEYLASL 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                137 FPDSLIVKGFNVVSAWALQLGPKDASRQVYICSNNIQARQQVIELARQLNFIPIDLGSLS 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            337 HSLSYSL------FAIINHAFK----ISNK------QLYWKFGIASITVLCVL 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             375 AVTSIPSVSNALNWREFSFIQSTLGYVALLI---STFHVLIY-GWKRAFE------EE 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels 142; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    183 IIAVFFHMSHYNGLNRALFASRFVNYIRGHFVLPTFLVD----KHANHFKFLNVEVFTGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   316 H-VAYSLCLPMRRSERYLFLNMAYQQVHANIENSWNEEEVWRIEMYISFGIMSLGLLSLL
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL). SIMILARITY: BELONGS TO THE FRE / CYBB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                             Electron transport; Transmembrane; Iron transport; FAD; NAD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51; Mismatches 119;
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POLY-LEU.
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SIGNAL 17
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                                                                                                                                                                                                                                                        EMBL; 247973; CAA88006.1; -.
EMBL; 273156; CAA97503.1; -.
SGD; S0003974; FREG.
INTERPRO; IPR002916; -.
PFAM; PF01794; Ferric_reduct; 1.
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Matches 72; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FERRIC REDUCTASE TRANSMEMBRANE COMPONENT
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                                                                                                                                                                                                                                      Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yeast 11:1281-1288(1995).
-! -CRACTOR: FAD (PROBABLE).
-! -SAGTOR: FAD (PROPABLE).
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
-!- SIMILARITY: BELONGS TO THE FRE / CYBB FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Casamayor A., Aldea M., Casas C., Herrero E., Gamo F.J.,
Lafuente M.J., Gancedo C., Arino J.;
"DNA sequence analysis of a 13 kbp fragment of the left
chromosome XV containing seven new open reading frames."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Electron transport; Transmembrane; Iron transport; FAD;
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2384480E9289C16F CRC64;
                                                                                                     15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
FERRIC REDUCTASE TRANSMEMBRANE COMPONENT 7 PRECURSOR.
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                                                        629 AA
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MEDLINE=96132030; PubMed=8553699;
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FRE7_YEAST
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SEQUENCE
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Jiang X., Dreano M., Buckler D.R., Cheng S., Ythier A., Wu H., Hendrickson W.A., el Tayar N.;
"Structural predictions for the ligand-binding region of glycoprotein hormone receptors and the nature of hormone-receptor interactions.";
Structure 3:1341-1353(1995)
-:- FUNCTION: RECEPTOR FOR FOLLICLE STIMULATING HORMONE. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE
   --LIYGWKRAFEEEYYR- 425
                                   FYEIFLQLHW----ILAVGFYISLF---YHVYPELNSHMYLVATIVVW---FAQLFYRL 311
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Kelton C.A., Cheng S.V., Nugent N.P., Schweickhardt R.L.,
Rosenthal J.L., Overton S.A., Wands G.D., Kuzeja J.B., Luchette C.A.,
                                                                                                                                                                                                                                                                                                                                                                                         01-WAR-1992 (Rel. 21, Created),
01-UNL-1994 (Rel. 29, Last sequence update)
01-CTT-2000 (Rel. 40, Last annotation update)
FOLLICLE STIMULATING HORMONE RECEPTOR PRECURSOR (FSH-R) (FOLLITROPIN
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ALTERNATIVE PRODUCTS: A SHORT FORM OF THE TESTICULAR PROTEIN IS
PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE. THE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ecloning of the human follicle stimulating hormone receptor and expression in COS-7, CHO, and Y-1 cells."; Cell. Endocrinol. 89:141-151(1992).
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Characterization of the S' flanking region of the human follicle-
stimulation bormone recentor dane ".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Minegish T., Nakamura K., Takakura Y., Ibuki Y., Igarashi "Cloning and sequencing of human FSH receptor cDNA.";
Biochem. Biophys. Res. Commun. 175:1125-1130(1991).
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Kowalski K.I., Perlas E.A., Hsueh A.J.;
Submitted (XXX-1992) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  695 AA
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Mol. Cell. Endocrinol. 102:93-102(1994).
--SVSNALNWREFSFIQSTLGYVALLISTFHV-
                                                                                                                                                                                                                                                                                                                                      PRT;
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MEDLINE=96363672; PubMed=8747461;
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Mammalia; Eutheria; Primates;
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                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MISSING (IN SHORT TESTICULAR ISOFORM).
MISSING (IN SHORT TESTICULAR ISOFORM).
  SHOWN HERE IS THAT OF THE LONG TESTICULAR PROTEIN.
TISSUE SPECIFICITY: SERTOLI CELLS AND OVARIAN GRANULOSA CELLS.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 (POTENTIAL).
CYTOPLASHIC (POTENTIAL).
N.LINKED (GLCNAC. ) (POTENTIAL).
N.LINKED (GLCNAC. .) (POTENTIAL).
N.LINKED (GLCNAC. .) (POTENTIAL).
N.LINKED (GLCNAC. .) (POTENTIAL).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PSSO562; G_RROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Signal; Phosphorylation; Repeat; Leucine-repeat; Alternative splicing;
                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
FOLLICLE STIMULATING HORMONE EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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T -> A (IN REF. 1).
N -> S (IN REF. 1).
723B8E71F76D2CD5 CRC64;
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N -> T (I
EL -> AV
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PRINTS; PR01143; FSHRECEPTOR.
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                                                                                                                                              EMBL; M65085; AAA52477.1; -.
                                                                                                                                                       EMBL; S59900; AAB26480.1; -. EMBL; M95489; AAA52478.1; -. EMBL; X68044; CAA48179.1; -. EMBL; S73199; AAB32071.1; -.
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78294 1
                                    FSH/LSH/TSH SUBFAMILY.
                                                                                                                                                                                                                                                                                                                               PFAM; PF00001; 7tm 1; 1.
PFAM; PF00560; LRR; 4.
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INTERPRO; IPR000372;
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INTERPRO; IPR002131;
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PDB; 1XUN; 15-MAY-97.
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197
295
307
680
695 AA;
                                                                                                                                                                                                                      GCR_0071; -GCR_0404; -GCR_0588; -GCR_0690; -
                                                                                                                                                                                                                                                                  MIM: 136435;
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17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        456 SVYTLTAITLERWHTITHAMQLDCKVQLRHAASVMVMGWIFAFAAALFPIFGISSYMKVS 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Porcine follicle-stimulating hormone receptor.";
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: RECEPTOR FOR FOLLICLE STIMULATING HORMONE. THE ACTIVITY
OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE
ADENYLATE CYCLASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  348 SWNEEEVWRIEMYISFGIMSLGLLSLLAVTSIPSVSNALNWRE------FSFIQSTL 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ------LCIGIYLLLIASVDIHTKSQYHNYAIDWQTGAGCDAAGFFTVFASEL 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----VLIYGWKRAFEEEYYRFYTPPNFV-LA 435
                                                                                                                   ---FNGTQLDELNLSDNNNLEELPNDVFHGASGPVILDISRTRIHSLPSYGLENLKKLRA 246
                                                                                                                                                                                                                                                                                                                                                                                                          247 RSTYNLKKLP-----TLEKLVALMEASLTYPSHCCAFANWRRQISELHPICNKSILRQE 300
                                                                                          ---KILIDVSNNMR 121
                                                                                                                                                                                122 INQYPESNAEYLASLFPDSLIVKGFNVVSAWALQLGPKDASRQVYICSNNIQARQQVIEL 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FSHR_PIG STANDARD; PRT; 695 AA.
P49059; 077514;
01-FEB-1996 (Rel. 33, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
01-CCT-2000 (Rel. 40, Last annotation update)
FOLLICLE STIMULATING HORMONE RECEPTOR PRECURSOR (FSH-R) (FOLLITROPIN
                                                                                                                                                                                                                                                                        182 ARQLNFIPIDLGSLSSAREIENLPLRLFTLWRGPVVVAISLATFFFLYSFVRDVIHPYAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                      -------PPWLETWLQCRKQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     361 GYNILRVLIWFISILAITGNIIVLVILTTSQYKLTVV----RFLMCNLAFAD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            306 G----LLSFFFAMVHVA-----YSLCLPMRRSERYLFLNMAYQQVHANIEN
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Sus.
  Length 695;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-OVARY;

MEDLINE-BOO11644; PubMed-7590277;

Remy J.J., Labbib-Mansais Y., Yerle M., Bozon V., Couture Pajot E., Grebert D., Salesse R.;
                                                                                                                                                                                                                            157 IH-----TIERNSFVGLSFESVILWL---NKNGIQEIHNCA---
                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wang Y.F., Meyer K.B., Schmidt K., Wan S.J., Degen S.J.F.
la Barbera A.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          expression and chromosomal localization of the gene."; Gene 163:257-261(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
    DB 1;
                                              148;
                                                                                        79 HEDALTKTNIIFVAIHREHYTSLWDLRHLLVG-------
4.6%; Score 107.5; I
larity 17.0%; Pred. No. 1.6;
Conservative 77; Mismatches
                                                                                                                                                                                                                                                                                                                                                                NQQSDFYKIPIEIVNKTL-PIVAITLLSLVY--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                436 LVLPSIVILDLLQL 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         516 ICLPMDIDSPLSQL 529
                       Similarity
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TISSUE=OVARY;
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  Query Match
Best Local Simi
Matches 84;
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240 ARNQOSDFYKIP----IEIVNKTL-
               4.48;
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                                  Conservative
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                        Similarity
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                                  91;
             Query Match
Best Local S
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                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
FSH/LSH/TSH SUBFAMILY.
                                                                                                                                                                                                                                                                                                                          FOLLICLE STIMULATING HORMONE RECEPTOR
                                                                                                                                                                                                                                                PRINTS; PR00373; GLVCHORMONER.
PRINTS; PR0143; FSHRECEPTOR.
PROSITE; PS00237; G_PROTEIN_RECEP_FL_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_FL_2; 1.
G_Protein coupled_receptor; Transmembrane; Glycoprotein; Signal;
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N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
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7 (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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E9EBEDB29C79C450 CRC64;
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EXTRACELLULAR (POTENTIAL)
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2 (POTENTIAL).
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STGNAL 1
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EMBL; AF025377; AAC24981.1; -
HSSP; P23945; 1XUN.
                                                                                                                                                       GCRDB, GCR_1561; --
INTERPRO; IPRO00276; --
INTERPRO; IPRO00372; --
INTERPRO; IPRO01611; --
INTERPRO; IPRO02131; --
                                                                                                                                                                                                                   PFAM; PF00001; 7tm_1; 1.
PFAM; PF00560; LRR; 4.
PFAM; PF01462; LRRNT; 1.
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695 AA;
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21;

    180 ELARQLNFIPIDLGSLSSAREIENLPLRLFTLWRGPVVVAISLATFFFLYSFVRDVIHPY 239

                                                                                                                                                                                                                                                                                                                                                                                                     ----FNGTQLDELNLSDNDNLEELPNDVFQGASGPVILDISRTRIHSLPSYGLENLKKL 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RAKSTYNLKKLPSLEKFVILMEASLTYPSHCCAFANWRRQISDLHPICNKSILRQEVDVM 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----SLVYLAGLLAAAYQLYYGTKYRRF-------PPWLETWLQCRKQLG--- 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EEVWRIEMYISFGIMSLGLLSLLAVTSIPSVSNALNWRE-----FSFIQSTLG--- 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ------LCIGIYLLLIASVDIHTKTQYHNYAIDWQTGAGCDAAGFFTVFASELSVYT 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----VLIYGWKRAFEEEYYRFYTPPNFV-LALVLP 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T.,
                                                                                                                                                                                 77 THHEDALTKTNIIFVAIHREHYTSLWDLRHLLVG---------KILLDVSNN 119
                                                                                                                                                                                                                                                                             120 MRINQYPESNAEYLASLFPDSLIVKGFNVVSAWALQLGPKDASRQVYICSNNIQARQQVI 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---PIVAITLL----- 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --YSLCLPMRRSERYLFLNMAYQQVHANIENSWNE 351
                                                Gaps
                                                                                           LPNG-INGIKDARKVTVGVIGSGDFAKSLTIRLIRCGYHVVIGSRNPKFASEFFPHVVDV 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.,
STRAIN-KIZ. / MG1625,
STRAIN-KIZ. / MG1627,
FUDMEDLINE-97426617;
FUDMEDLINE-97426617;
FUDMERT F.R., PLUNKETT G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
                                                                                                                                    61 IPKGAFSGFGDLEKI-----EISQNDVLEVIEAN----VFSNLPKL-----
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Escherichia
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P31122; P77353; P76883;
01-7011-1993 (Rel. 26, Created)
01-NV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
HYPOTHETICAL 42.5 KDA PROTEIN IN UXAB-MARR INTERGENIC REGION.
Length 695;
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                                                Indels
Score 104.5; DB 1;
Pred. No. 2.6;
91; Mismatches 169;
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MEDLINE=97251357; PubMed=9097039;
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SLC17A1 OR NPT
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                                                                                                                                                                                                                                                                                                                -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE
    Kasal H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito I Sampel G., Seki Y., Sivasundaram S., Tagami H., Takeda J., Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.; As 570-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 28 0-40.1 min region on the linkage map.";
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                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: STRONG, TO H.INFLUENZAE H10135.
SIMILARITY: TO S.LIVIDANS CHLORAMPHENICOL RESISTANCE PROTEIN
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                                                                                                                                                                                                                             Cohen S.P., Haechler H., Levy S.B.;
"Genetic and functional analysis of the multiple antibiotic resistance (mar) locus in Escherichia coli.";
J. Bacteriol. 175:1484-1492(1993).
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EG11636; YDEA.
                                                                                                                                                                                     SEQUENCE OF 217-396 FROM N.A. MEDLINE-93186717; PubMed-8383113;
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15-UUL-1998 (Rel. 36, Last annotation update)
RENAL SODIUM-DEPENDENT PHOSPHATE TRANSPORT PROTEIN I (SODIUM/PHOSPHATE COTRANSPORTER I) (NA(+)/PI COTRANSPORTER I) (RENAL SODIUM-PHOSPHATE TRANSPORTER I) (RENAL NA+-DEPENDENT PHOSPHATE COTRANSPORTER I).
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Am. J. Physiol. 268:F1038-F1045(1995).
-I- FUNCTION: IMPORTANT FOR THE RESORPTION OF PHOSPHATE BY THE KIDNEY.
MAY BE INVOLVED IN ACTIVELY TRANSPORTING PHOSPHATE INTO CELLS VIA
NA+ COTRANSPORT IN THE RENAL BRUSH BORDER MEMBRANE.
-I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PHOTEIN.
                                                                                                                                                                                                                                                                        240 ARN---QQSDFYKIPIEIVNKTLPIVAITLLSLVYLAGLLAAAYQLYYGTKYRRFPPWLE 296
                                                                                                                                                                                                                                      ---ALNWREFSFIOST 397
                                                                                                                297 TWLQCRKQLGLLSFFFAMVHVAYSLCLPMRRSERYLFLNMAYQQVHANIENSWNEEEVWR
                                                                                                                                                                    -----ALVSTAIALLLVCLALLLPAANSE-----IHLGVLSIF----WG
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Chong S.S., Kozak C.A., Liu L., Kristjansson K., Dunn S.T.,
Bourdeau J.E., Hughes M.R.;
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                                                         236 VQNIAGESANF----
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465 AA;
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                                                                          16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :| : | : | : | : | : | 38 | 136 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          188 GFICDLLGWPMVFYIFGIVGCVLSLSWFFLFFDDPKD--HPYMSSSEKDYIISSLMQQAS 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SGRQSLPIKAMLKSLPLWAIILNSFAFIWSNSLLVTYTPTFISTVLHVNVRENGLLSSLP 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --LVYLAGLLAAAYQLYYGTKYRRPPPWLETWLQCRKQLGLLSFFFAMVHVAYSLCLPMR 326
                                                                                                                                          110 GKILIDVSNNMRINQYPESNAEYLASLFPDSLIVKGFNVVSAWALQLGPKDA---SRQVY 166
                                                                                                                                                                                                                                                                                                                                                                                                                                      306 YLLAYICGILAGOMSDFFLTRK-----IFSIVTVRKLFTTLGFFCPVIFIMCLLYLSYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      327 RSERYLFLNMAYQQVHANIENSWNEEEVWRIEM---YISF--GIMSL-----GLLSLLAV
                                                                                                                                                                                                                                                                                        167 ICSNNIQARQQVIELARQLNFI----PIDLGSLSSAREIENLPLRLFTLWRGPVVV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             248 ---YKIPIEIVNKTLPIVAITLLS------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
4.4%; Score 103; DB 1; Length 465;
18.7%; Pred. No. 2.1;
tive 64; Mismatches 142; Indels 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: THE RF3 PROTEINS ARE RELATED TO THE MATURASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=87280035; PubMed=2440860; Seraphin B., Simon M., Faye G.; The mitochondrial reading frame RF3 is a functional gene in Saccharomyces uvarum."; J. Biol. Chem. 262:10146-10153(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                377 TSIPSVSNALNWREFSFIQSTLGYVALLISTFHVL----IYGWKR 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 416 GLILNQDPEYAWHKISFLMAGINVTCLV---FYFLFAKGEIQDWAK 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57863 MW; ECB416C51DFFDA6D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saccharomyces bayanus (Yeast) (Saccharomyces uvarum).
Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1988 (Rel. 09, Last sequence update) 30-MAY-2000 (Rel. 39, Last annotation update) MATURASE-LIKE RF3 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           476 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INTERPRO; IPR001982; -.
PFAM; PF00961; Intron_maturase; 1.
Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saccharomycetaceae; Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1988 (Rel. 09, Created)
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                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           476 AA;
Query Match
Best Local Similarity
Matches 76; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A28439;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RF3_SACBA
P05512;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J. Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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Length 476;

Score 100; DB 1; Pred. No. 3.6;

4.38;

Query Match Best Local Similarity

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  12;
                                                                                                                                                                                                                   - RPSYVIS-QVETRKELIYLIQE----SFDL-SISNVKKVGNRKLKDFKLFTRTTDELMK 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          109 VGKIL-----IDVSNNMRINQYPESNAEYLASLFPDSLIVKGFNVVSAWALQLGPKDAS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RQVYICSNNIQAR----QQVIELARQLNFIPIDLGSLSSAREIENLP-LRLFTLWRGPV 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80 QQHWVSESLIYQRVFVGCQVFLTGALVLAFMASDLLFYIAFESTLLDTLMLITRW-GAQ 138
                                                            222 LATFFLYSFVRDVIHPYARNQQSDFYKIP----IEIVNKTLPIVAITLLSLVYLAGLLA 277
                                                                                                                                                                                                                                                                                                104 LRHLLVGKILIDVSNNMRINQYPESNAEYLASLF--PDSLIVKGFNVVSAWALQLGPKDA 161
    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29 VGSVLLMLPATVLVNMNMTI----SNVSYMMT---SDFVSLGLTVLSIWLLPL-MLLAS
                                                                                                                                                                                           162 SRQVYICSNNIQARQQVIELARQLNFIPIDLGSLSSAREIENLPLRLFTLWRGPVVVAIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
Branchiostoma.
  :99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Spruyt N., Delarbre C., Gachelin G., Laudet V.;
"Complete sequence of the amphioxus (Branchiostoma lanceolatum)
mitochondrial genome: relations to vertebrates.";
Nucleic Acids Res. 26:3279-3285(1998).
-!- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 452;
                                      NPKFASEFFPHVVDVTHHEDALTKTNI - - - - IFVAIHREHYT - - - - - - -
  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Branchiostoma lanceolatum (Common lancelet) (Amphioxus).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     e; Mitochondrion.
4067DB59EC184C7A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4 (EC 1.6.5.3).
                                                                                                                                     303 INNKLPIKNIMDIKNNYWLAGFTAADGSFLSSMYNPKDTLLFKDM-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4.2%; Score 99.5; DB 1; 20.1%; Pred. No. 3.7; Live 56; Mismatches 139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     452 AA
48; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=98292550; PubMed=9628930;
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PFAM; PF001059; oxidored_q5_N; 1.
Oxidoreductase; NAD; Ubiquinone;
SEQUENCE 452 AA; 49940 MW; 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-DEC-1998 (Rel. 37, Created)
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Best Local Similarity 20.1%
Matches 95; Conservative
  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INTERPRO; IPR000260; -. INTERPRO; IPR001750; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ND4 OR NAD4 OR NADH4.
                                                                                                                                                                                                                                                                                                                                                  278 AAYQLYYGTKY 288
                                                                                                                                                                                                                                                                                                                                                                                       452 DNYDYYYYNKY 462
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mitochondrion.
  52;
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  Matches
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                                                                324
                                                                                                                                                                                              SLIAYSSVGHMALVVGGVLTGVAWGYNGAMVLMIAHGLVSSCLFCLANLWYERSSTRNLS 340
                                                                                                                                                                                                                                                 341 GSRGLIMIFPLISLGWFLMSLMNMALPPAINLFGELVAMVALYNWSPYSIVYMSLG--AV 398
                                                                                                                                                                                                                                                                                                                                                                GP68_HUWAN STANDARD, PRT; 365 AA.
Q15743; Q1334;
15-JUL-1998 (Rel. 36, Created)
16-JUL-1998 (Rel. 36, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
PUTATIVE G PROTEIN-COUPLED RECEPTOR GFR68 (OVARIAN CANCER G PROTEIN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
                                                                                                                                                                      ---HANIE-----NSWNEEEVWR---
          217 VVAISLATFFFLYSFVRDVIHPYARNQQSDFYKIPIEIVNKTLPIVAITLLSLVYLAGLL
                                    -----GSLPLL-ICLIGQYQMVGSL
                                                                                       174 ALDLSYEGVFQLSYLVNF----W---WVGC----ILAFLVKLPLYGVHLWLPKAHVEA
                                                                                                                                         221 PIAGSMVLAGVLLKLGGYGMMRVSLMWGATAMLSSEVFLALALWGIVVMGGICLRQTDLK
                                                              A-----AAYQLYYGTKYRRFPPWLETWLQCRKQLGLLSFFFAMVHVAYSLCLP-----
                                                                                                                                                                                                                        --IEMYISFGIMSLG--LLSLLAVTSIPSVS-----NALNWREFSFIQSTLGYVAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Xu Y., Casey G.;
"Identification of human OGR1, a novel G protein-coupled receptor
that maps to chromosome 14.";
Genomics 35:397-402(1996).
                                                                                                                                                                                                                                                                                         404 LISTFHVLIYG---WKRAFEEEYYRFY--TPPNFVLAL--VLPSIVILDLLQL 449
                                                                                                                   ----MRRSERYLFLNM-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-OVARIAN CARCINOMA;
MEDLINE-96299795; PubMed-8661159;
                                                                                                                                                                                                                                                                                                                                                                                                                                           COUPLED RECEPTOR 1) (OGR-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NOT DETECTABLE IN OVARY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U48405; AAC50596.1; -
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                                    139 KERYQAGTYFMFFTLV---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A
                                                                                                                                                                    ---AYQQV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                           GPR68 OR OGR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       601404;
                                                                                                                                                                                                                                                                                                                                                    GP68_HUMAN
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INTERPRO; IPR000276; -. PFAM; PF00001; 7tm_1; 1

MIM;

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POLG_YEFV1 STANDARD; PRT; 3411 AA.

POLG_YEFV1

PO1314; O42028;

PO3314; O42028;

21-JUL-1986 (Rel. 01, Created)

21-JUL-1986 (Rel. 01, Last sequence update)

15-DEC-1998 (Rel. 37, Last annotation update)

15-DEC-1998 (Rel. 37, Last annotation update)

15-DEC-1998 (Rel. 37, Last annotation update)

PROPEDIN (ENVELOPE PROTEIN N): MAJOR ENVELOPE PROTEIN; MATRIX PROTEIN (ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEIN SS), NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED FINA POLYMERASE (EC 2.7.7.48) (NS5)].

Yellow fever virus (strain 17D).

Viruses; SSRNA positive-strand viruses, no DNA stage; Flaviviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     314 MVHVAYSLCLPMRRSERYLFLNMAYQQVHANIENSWNEEEVWRIEMYISFGIMSLGLLSL 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          255 VNKTL-PIVAITLLSLVYLAGLLAAAYQLYYGTKYRRPPPWLETWLQCRKQLGLLSFFFA 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65 VADLFYICSLPFW------LQYVLQHDNWSHGDLSCQVCGILLYENIYI-SVGFLCC 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ::| :|:: :| ::| :|::: :| 115 ISVDRYLAVAHPERIEDENQHRVCFE 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19 IHQTLAPVVYVTVL----VVGFPANCLSLYFG------YLQ--IKARNELGVYLCNLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: THE SMALL PROTEINS NS2A, NS2B, NS4A AND NS4B ARE HYDROPHOBIC, SUGGESTING A POSSIBLE MEMBRANE-RELATED FUNCTION. NS3 AND NS5 MAY PLAY A ROLE IN THE VIRAL RNA REPLICATION.
                                                                                                                                                                                                                                                                                                                                                                                . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Surduss J.H.; , 
"Nucleotide sequence of yellow fever virus: implications for 
flavivirus gene expression and evolution."; 
Science 229:726-733(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rice C.M., Lenches E.M., Eddy S.R., Shin S.J., Sheets R.L., Strauss J.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 365;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
           G_PROTEIN_RECEP_F1_1; 1.
G_PROTEIN_RECEP_F1_2; 1.
receptor; Transmembrane; Glycoprotein.
21 EXTRACELLULAR (POTENTIAL).
                                                                                         1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                      7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
N-LINKED (GLCNAC. . . ) (PC
                                                                                                                                                                                                                                                                                                                                                                                                                   G -> R (IN REF. 2).
S -> T (IN REF. 2).
05919AFD5B842CCD CRC64;
                                                                                                                                                                                                       4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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                                                                                                                                                                                                                                               5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4.2%; Score 99; DB : 22.6%; Pred. No. 3.1; Live 37; Mismatches
                                                                                                                                                                                                                                                                                     6 (POTENTIAL)
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MEDLINE-85272570; Pubmed-4023707;
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PR00237; GPCRRHODOPSN
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284
365
172
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Best Local Similarity
Matches 48; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                       365 AA;
                 PS00237;
PS50262:
                                                     G-protein coupled
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159
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                 PROSITE;
PROSITE;
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                                                                                                                                                                                                                                             ΒX
SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS: PROFEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF PROTEIN C AND MRNA.
                                                                                                                                                                                                                                                                                                                                                                                        REMOVED FROM CAPSID PROTEIN C BY THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HELICASE (NS3)
NONSTRUCTURAL PROTEIN NS4A.
NONSTRUCTURAL PROTEIN NS4B.
RNA-DIRECTED RNA POLYMERASE (NS5).
                                                                                                                                                                                                                                                                                                                                                                                                                                            NONSTRUCTURAL PROTEIN NS1.
NONSTRUCTURAL PROTEIN NS2A.
NONSTRUCTURAL PROTEIN NS2B.
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                                                                                                                                                                                                                                                                                                                                                                                                CELLULAR AMINOPEPTIDASE CAPSID PROTEIN C.
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ATP (POTENTIAL).
DEAH BOX.
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BY SIMILARITY.
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N-LINKED (GLCNAC.
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                                                                                                                                                                                 INTERPRO; IPR000404; -.
INTERPRO; IPR000487; -.
INTERPRO; IPR000752; -.
INTERPRO; IPR001122; -.
INTERPRO; IPR001152; -.
INTERPRO; IPR001158; -.
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                                                                                                                                                       INTERPRO; IPR000069;
                                                                                                                                                                  INTERPRO; IPR000208;
                                                                                                                                        1SVB
                                                                                                                              PIR; A03914; GNWVY
HSSP; P14336; 1SVB
                                                                                                                                                MEROPS; S07.001;
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. .) (POTENTIAL)

(GLCNAC.

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                                                                                                                                                                     20;
                                                                                                                                                                                                                                    1280 PLMALLTPVTMAEVRLAAMFFCAVVIIGVLHQNFKDTS------MQKTIPLVALTL 1329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LAFQEMENFLGPIAVGGLLMMLVSVAGRVDGLELKKLGEVSWEEEAEISGSSARYDVALS 1433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
115-DEC-1998 (Rel. 37, Last annotation update)
GENOME POLYPROTEIN (CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX
PROTEIN (ENVELOPE PROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL
PROTEINS NS1, NS2A, NS2A, NS2A, AND NS4B; HELICASE (NS3); RNA-DIRECTED
RNA POLYMERASE (EC 2, 7, 7, 48) (NS5).
Fellow fever virus (strain Pasteur 17D-204).
                                                                                                                                                                                                                                                                                                                                                                              RLFTLWRGPVVVAISLATFFFLYSFVRDVIHPYARNQQSDFYKIPIEIVNKTLPIVAITL 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                              LSLVYLA----GLLAAAYQLYYGTKYRRFPPWLETWLQCRKQLGLLSFFFAMVHVAYSLC 322
                                                                                                                                                                                                          107 LLVGKI-LID-----VSNNMRINQYPE-SNAEYLA----SLFPDSLIVKGFNVVSAWA- 153
                                                                                                                                                                                                                                                                                            154 ----LQLGPKDASRQVYICSNNIQARQQVIELARQLNFIPIDLGSLS--SAREIENLPL 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LPMRRSERYL-----FLNMAYQQVHANI-----ENSWNEE-EVWRIEMYISFGIM 366
                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Flavivirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dupuy, A., Despres P., Cahour A., Girard M., Bouloy M.;
"Nucleotide sequence comparison of the genome of two 17D-204 yellow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEIC ACIDE RES. 17:3989-3989(1989).
-!- FUNCTION: THE SMALL PROTEINS NS2A, NS2B, NS4A AND NS4B ARE HYDROPHOBIC, SUGGESTING A POSSTBLE MEMBRARNE-REATED FUNCTION.
NS3 AND NS5 AND YEAY A ROLE IN THE VIRAL RNA REPLICATION.
-!- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY LIPOPROTEIN BYNELOPE: THE ENVELOPE CONSISTS OF TWO PROTEINS:
PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF PROTEIN C AND MRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1330 TSYLGLTOPFLGLCAFLATRIFG --- RRSIPVNEA - LAAAGLVGVLA--------G
  (GLCNAC. . .) (POTENTIAL). (GLCNAC. . .) (POTENTIAL). (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                     88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1434 EQGEFKLLSEEKVP-----WDQ--VVMTSLALVGAALHPFALLLVLAGW 1475
                                                                                                                        DB 1; Length 3411; 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SLGLLSLLAVTSIPSVSNALNWREFSFIQSTLGYVALLISTFHVLIY - - GW
N-LINKED (GLCNAC. . .) (POTINED (GLCNAC. . .) (POTINED (GLCNAC. . .) (POTINED (GLCNAC. . .) (POTINE) (W) 680E0FACD23DCFA6 CRC64;
                                                                                                                                                                   55; Mismatches 130;
                                                                                                                          4.2%; Score 98; 22.2%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X15062; -; NOT_ANNOTATED_CDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE-89282413; PubMed-2734112;
Dupuy,A., Despres P., Cahour A., G
                                                              379512
                                                                                                                                       Best Local Similaria,
...-rhes 78; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
2320
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2467
2320 23:
2346 23:
2467 24:
3411 AA;
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  CARBOHYD
CARBOHYD
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POLG_YEFV2
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PFAM; PF01570; Flavi_propep; 1.
Polyprotein; Glycoprotein; Transferase; RNA-directed RNA polymerase; Core protein; Coat protein; Envelope protein; Helicase; ATP-binding; Iransmembrane; Nonstructural protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REMOVED FROM CAPSID PROTEIN C BY THE CELLULAR AMINOPEPTIDASE.
CAPSID PROTEIN C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HELICASE (NS3).
NONSTRUCTURAL PROTEIN NS4A.
NONSTRUCTURAL PROTEIN NS4B.
RNA DIRECTED RNA POLYMERASE (NS5).
ATP (POTENTIAL).
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NONSTRUCTURAL PROTEIN NSI.
NONSTRUCTURAL PROTEIN NS2A.
NONSTRUCTURAL PROTEIN NS2B.
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PFAM: PF00869; Flavi_glycoprot; 1
PFAM: PF00949; Flavi_helicase; 1.
PFAM: PF01570; Flavi_propep; 1.
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F01349; Flavi_NS4B;
F00972; Flavi_NS5; 1
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2346 234
2467 246
3411 AA;
              PIR; S07757; GNWVYP
                                                                                                                                                       INTERPRO; IPRO00487
INTERPRO; IPRO0152
INTERPRO; IPRO01122
                               P14336; 1SV
S; S07.001;
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INTERPRO;
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SEQUENCE
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Ouery Match

4.2%; Score 98; DB 1; Length 3411;

Best Local Similarity 22.2%; Pred. No. 49;

Matches 78; Conservative 55; Mismatches 130; Indels 88; Gaps 20;

Qy 107 LLVGKI-LID-----VSNNMRINQYPE-SNAEYLA-----SLPPDSLIVKGFNVVSAWA-153

1171 MLVGQVTLLDLLKLTVAVGLHFHEMNNGGDAMYMALIAAFSIRPGLLI--GFGLRTLMSP 1228

Qy 154 -----LOLGPKDASRQVYICSNNIQARQOVIELARQLNFIPIDLGSLS--SAREIENLPL 206
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KASNTIL 1279	PIVAITL 266	MOKTIPLVALTL 1329	HVAYSLC 322	1373	MYISFGIM 366	: ARYDVALS 1433	115	1475
: : :: :: :: :: :: :: :: :: :: ::	NDVIHPYARNQOSDFYKIPIEIVNKTI		REPPWLETWLOCRKOLGLLSFFFAM	RESIPVNEA-LAAAGLVGVLA	NITENSWNEE-EVWRIEN	: RVDGLELKKLGEVSWEEEAEISGSSA	IQSTLGYVALLISTFHVLIYGW 4	: : : : : : : :
1229 RERLYLTLGAMWEIALGGVMGGLWKYLNAVSLCILTINAVASRKASNTIL 1279	207 RLFTLWRGPVVVAISLATFFFLYSFVRDVIHPYARNQQSDFYKIPIETVNKTLPIVAITL 266	1280 PLMALLTPVTMAEVRLAAMFFCAVVIIGVLHQNFKDTSMQKTIPLVALTL 1329	267 LSLVYLAGLLAAAYQLYYGTKYRRPPWLETWLQCRKQLGLLSFFFAMVHVAYSLC 322	1330 TSYLGLTQPFLGLCAFLATRIFGRRSIPVNEA-LAAAGLVGVLAG 1373	323 LPMRRSERYLFLNMAYQOVHANIENSWNEE-EVWRIEMYISFGIM 366	1374 LAFQEMENFLGPIAVGGLIAMLVSVAGRVDGLELKKLGEVSWEEEAEISGSSARYDVALS 1433		1434 EQGEFKLLSEEKVPWDQVVMTSLALVGAALHPFALLLVLAGW 1475
1229	207	1280	267	1330	323	1374	367	1434
QQ	Qy	QQ	Qy	qq	QY	qq	QY	QQ

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